

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2001, 16:12:48 ; Search time 12.3 Seconds
(without alignments)
1191.993 Million cell updates/sec

Title: US-09-455-486-6

Perfect score: 2351

Sequence: 1 MESISMWGPKSLEFCLPN.....ALVLPISIVLDLQLCRYPD 454

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Length	ID	Description
1	133	5.7	223	1 FARE_METJA	Q58896 methanococ
2	120.5	5.1	232	1 FARE_METH	O26350 methanobact
3	111.5	4.7	695	1 FSHR_MACFA	P32212 macaca fasc
4	109	4.6	693	1 FSHR_CHICK	P79763 gallus gall
5	109	4.6	712	1 FRE6_YEAST	Q12473 saccharomyc
6	107.5	4.6	629	1 FRE7_YEAST	Q12333 saccharomyc
7	107.5	4.6	695	1 FSHR_HUMAN	P23945 homo sapien
8	104.5	4.4	695	1 FSHR_PIG	P49059 sus scrofa
9	104	4.4	396	1 YDEA_ECOLI	P31122 escherichia
10	103	4.4	465	1 NPT1_MOUSE	Q61983 mus musculu
11	100	4.3	476	1 RF3_SACBA	P05512 saccharomyc
12	99.5	4.2	452	1 NU4M_BRALA	O79421 branchiosto
13	99	4.2	365	1 GP68_HUMAN	Q15743 homo sapien
14	98	4.2	3411	1 POLG_YEFV1	P03314 y genome po
15	98	4.2	3411	1 POLG_YEFV2	P19901 y genome po
16	97.5	4.1	695	1 FSHR_BOVIN	P35376 bos taurus
17	97	4.1	692	1 FSHR_RAT	P20395 rattus norv
18	96.5	4.1	686	1 FRE1_YEAST	P32791 saccharomyc
19	96	4.1	261	1 PHSC_ECOLI	P77409 escherichia
20	95	4.0	393	1 NUCC_ARATH	P56753 arabidopsis
21	94.5	4.0	492	1 SECY_CYAPA	P25014 cyanophora
22	94.5	4.0	695	1 FSHR_SHEEP	P35379 ovis aries
23	93.5	4.0	452	1 NU4M_BRAFL	O47423 branchiosto
24	93.5	4.0	499	1 GSHR_PLAF7	O15770 plasmodium
25	93.5	4.0	1233	1 VL1_REOVD	P15024 reovirus (t
26	93	4.0	388	1 HMC3_DESVH	P33390 desulfovibr
27	93	4.0	459	1 NU4M_BOVIN	P03910 bos taurus
28	93	4.0	521	1 Y725_CAEEL	Q10934 caenorhabdi
29	92.5	3.9	490	1 GFR1_CHICK	P46896 gallus gall
30	92.5	3.9	883	1 YHL6_YEAST	P38781 saccharomyc
31	92.5	3.9	1769	1 YJK9_YEAST	P42945 saccharomyc
32	92.5	3.9	2037	1 FAS1_CANAL	P34731 c fatty aci
33	91.5	3.9	495	1 TPS1_YEAST	Q00764 s alpha,alp

ALIGNMENTS

RESULT 1

F4RE_METJA
ID F4RE_METJA STANDARD; PRT; 223 AA.

AC Q58896;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE PUTATIVE F420-DEPENDENT NADP REDUCTASE (EC 1.-.-.-).

GN MJ1501.

OS Methanococcus jannaschii.

OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;

CC Methanococcus.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

RX MEDLINE=96337999; PubMed=8688087;

RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,

RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Reich C.I.,

RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

RA "Complete genome sequence of the methanogenic archaeon, Methanococcus

jannaschii.";

RL Science 273:1058-1073(1996).

CC -!- FUNCTION: CATALYSES THE REDUCTION OF F420 WITH NADP(+) AND THE

REDUCTION OF NADP(+) WITH F420H(2). PROBABLY COUPLES THE NADP-

DEPENDENT OXIDATION OF THE ALCOHOL TO THE ALDEHYDE WITH DE F420-

DEPENDENT REDUCTION OF CO(2) TO METHANE (ANABOLIC FUNCTION) (BY

SIMILARITY).

CC -!- CATALYTIC ACTIVITY: NADPH + COENZYME F420 = NADP(+) + REDUCED

COENZYME F420.

CC -!- SIMILARITY: TO M.ORGANOPHILUM F420-DEPENDENT NADP REDUCTASE.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL; U67591; AA989514.1; .

DR TIGR; MJ1501; .

KW Hypothetical protein; Oxidoreductase; NADP.

SQ SEQUENCE 223 AA; 24068 MW; 2370BBBD6F5BBD3D9 CRC64;

Query Match

Best Local Similarity 5.7%; Score 133; DB 1; Length 223;

Matches 46; Conservative 52; Mismatches 78; Indels 34; Gaps 7;

QY 37 GSGDFAKSTILIRCGYHWVIGSRNPKFASEFFHVVDV-----THHEDALT 84

||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

FT CARBOHYD 268 268 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 4 4 G -> D (IN REF. 2).
 FT CONFLICT 88 88 G -> A (IN REF. 2).
 FT CONFLICT 140 140 K -> R (IN REF. 2).
 FT CONFLICT 174 174 I -> T (IN REF. 2).
 FT CONFLICT 191 191 N -> S (IN REF. 2).
 FT CONFLICT 329 329 V -> L (IN REF. 2).
 SQ SEQUENCE 693 AA; 78697 MW; 46F98699635A1BEC CRC64;

Query Match 4.68; Score 109; DB 1; Length 693;
 Best Local Similarity 17.28; Pred. No. 1.3;
 Matches 100; Conservative 72; Mismatches 173; Indels 238; Gaps 21;

QY 18 LPNG-INGIKDARKVTVG-----VIGSGDFAKSLTIRLIRGCVHWIGSRNPKFASEFFP 71
 Db 61 IPKCAFTGLDLEKIEISQNDALIEIGNVFSSL-----PKL----- 97

QY 72 HVVDVTHEDAL/TKNIIFVAIHREHYTS/LMDRLHLVG-----KILI 114
 Db 98 -----HEIRIERANKL-MKIDQDAFOHLP/LSLRYLLISNTGLSFLPVVHKVHSFQKVL 149

QY 115 DYSNNMRINQYPESNAEVLSPDLSLVKGFNVVSAWALQGLPKDASRQVYICNNIOA 174
 Db 150 DVQDNIIHIRTIERNTFMGLSS---ESVILR-----LNKNGIQE 184

QY 175 RQVIELARQLNFIPIDGLSSSARETENPLRLFTLWRGPPVVAISLATPFFYSFVRD 234
 Db 185 IKD-----HAFNGTCLDELNLSDNYNLEKLPKVFQGAIGPVVLDISKTRISFLPSHGLE 239

QY 235 VIHPYARNOQSDFYKPIEIVNKTLPVAILTLLSLVLAGL----- 275
 Db 240 FIKRLARSTYKLLKLP---DYNKFRSLTEANFTYPSHCFAFNTRKNTQNTPEYPCMSMSPA 297

QY 276 -----LAAAYQLYGTYK---RRF-----PPWLETWLCQR 302
 Db 298 KODLGEOTGRKKHRRSAAEDYISHTGRFGVNEFEDYGLCNEVVDVFCSPKPAFNPCE 357

QY 303 KQLG-----LLSFFFAVHVA-----YSLCLPMRRSERYFLNMAVQQVHAN 344
 Db 358 DIMGYNVLRLVILWFINILAITAGNTVLLIILISSQYKLTVP-----RFLMCLNLAFA 408

QY 345 IENSWNEEVEVRIEMYSIFGIMSLGLSLLAVTSPISVSNALNWE-----FSFIQ 395
 Db 409 -----LCIGIYLLFIASVDIQTSRYVNAIDWQTGAGCNAAGFTVFA 452

QY 396 STLGYVALLISTFH-----VLIYGNKRAF----- 419
 Db 453 SELSVYTLVTILRWHTIITYAMQLNRKVRRLRAVIIMVFGWMAFVALLPIFGISSYM 512

QY 420 -----EEYRYFTPTPNFVLAIVLPSIVILDLQLCRY 452
 Db 513 KVSICLPMHIETPSQAYV--IFLLVNLVAFVLCIYCIY 553

RESULT 5
 FRE6 YEAST
 ID FRE6.YEAST STANDARD; PRT; 712 AA.
 AC Q12473;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DE FERRIC REDUCTASE TRANSMEMBRANE COMPONENT 6 PRECURSOR.
 GN FRE6 OR YLL051C OR L0593.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 CC Saccharomycetaceae; Saccharomycetes.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C;
 RA Wedler H., Wambutt R.;
 RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
 CC -!- COFACTOR: FAD (PROBABLE).

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 -!- SIMILARITY: BELONGS TO THE FRE / CYBB FAMILY.
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 EMBL; Z47973; CAA88006.1; -;
 DR EMBL; Z73156; CAA97503.1; -;
 DR SGD; S0003974; FREG.
 DR INTERPRO; IPR002916; -;
 DR PFAM; PF01794; Ferric_reduct; 1.
 KW Electron transport; Transmembrane; Iron transport; FAD; NAD;
 KW Glycoprotein; Signal; Multigene family.
 FT SIGNAL 1 17 POTENTIAL.
 FT CHAIN 18 712 FERRIC REDUCTASE TRANSMEMBRANE COMPONENT 6.
 FT NP_BIND 493 499 FAD (POTENTIAL).
 FT TRANSMEM 168 188 POTENTIAL.
 FT TRANSMEM 245 265 POTENTIAL.
 FT TRANSMEM 288 308 POTENTIAL.
 FT TRANSMEM 329 349 POTENTIAL.
 FT TRANSMEM 361 381 POTENTIAL.
 FT TRANSMEM 388 408 POTENTIAL.
 FT TRANSMEM 417 437 POTENTIAL.
 FT TRANSMEM 478 498 POTENTIAL.
 FT TRANSMEM 550 570 POTENTIAL.
 FT DOMAIN 553 556 POLY-LEU.
 FT CARBOHYD 89 89 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 124 124 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 450 450 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 655 655 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 712 AA; 81989 MW; 5224F12B51544BAA CRC64;

Query Match 4.68; Score 109; DB 1; Length 712;
 Best Local Similarity 18.88; Pred. No. 1.3;
 Matches 72; Conservative 51; Mismatches 119; Indels 142; Gaps 17;

QY 88 IIFVAIHREHYTSL-----WDLRLLVGKILIDVSNMNRINQYPESNAEYLASL 136
 Db 183 IIAVFFHMSHYNGNLRALFASRFVNYIRGHVLPFLVD---KHANHFELNVEFTGL 238

QY 137 FPDSLVKGFNVVSAWALQGLPKDASRQVYICSNIOARQOVIELARQLNFIPIDGLSLS 196
 Db 239 MPNSL-----EAM----- 246

QY 197 SAREIENLPLRLFTLWRGPPVVAISLATPFFL-YSFVRDVIHPYARNOQSDFYKPIEIV 255
 Db 247 -----IIFGYTLANIIFLSYITIDPYNLIFNLSHQFTRL---LA 284

QY 256 NKTLPVIAITLLSLVLAGLAAAYQLYGYTKYRRFPWLETWLCQRKGLGLSFFFAWV 315
 Db 285 DRS-GILAFQFPFLIIFTARNSEFLFTGVKFNFSF-----ISFKHIGRIMVLNATI 336

QY 316 H-VAYSICLPMRRSERYFLNMAVQQVHANIEVSWNEEVEVRIEMYSIFGIMSLGLSLL 374
 Db 337 HSLSYSL-----FAIINHAFK-----ISNK-----QLYWKFGIASITVLCVL 373

QY 375 AVTSIPSVSNALNWRSEFSFQSTGLGYVALLI---STHVLIIY-GWKRAFE-----EE 422
 Db 374 LVLSGLGIVRK-----RHYEFFLYTHIILALLFFYCCWQHVIFNGKEMVIVVSLIWLGLEK 429

QY 423 YRYFYTPTNFVLAIVLPSIVILDL 446
 Db 430 LFRWN---ILQFRFPKATLINL 449

```

RESULT 6
ID FRE7_YEAST STANDARD; PRT; 629 AA.
AC Q12333;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE FERRIC REDUCTASE TRANSMEMBRANE COMPONENT 7 PRECURSOR.
GN FRE7 OR YOL152W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomycetes.
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=S288C / FY1679;
RX MEDLINE=96132030; PubMed=8553699;
RA Casamayor A., Aldea M., Casas C., Herrero E., Gamo F.J.,
RA Lafuente M.J., Gancedo C., Arino J.;
RT "DNA sequence analysis of a 13 kbp fragment of the left arm of yeast
RT chromosome XV containing seven new open reading frames.";
RL Yeast 11:1281-1288(1995).
CC -!- COFACTOR: FAD (PROBABLE).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -!- SIMILARITY: BELONGS TO THE FRE / CYBB FAMILY.
CC
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
DR EMBL; Z48239; CAA88276.1; -
DR EMBL; Z74894; CAA99174.1; -
DR SGD; S0005512; FRE7;
DR INTERPRO; IPR002916; -
DR PFAM; PF01794; Ferric_reduct; 1.
KW Electron transport; Transmembrane; Iron transport; FAD; NAD;
KW Glycoprotein; Signal; Multigene family.
FT SIGNAL 1 ?
FT CHAIN ? 629 FERRIC REDUCTASE TRANSMEMBRANE COMPONENT
FT FT 7.
FT NP_BIND 369 375 FAD (POTENTIAL).
FT TRANSMEM 46 66 POTENTIAL.
FT TRANSMEM 108 128 POTENTIAL.
FT TRANSMEM 168 188 POTENTIAL.
FT TRANSMEM 195 215 POTENTIAL.
FT TRANSMEM 238 258 POTENTIAL.
FT TRANSMEM 266 286 POTENTIAL.
FT TRANSMEM 293 313 POTENTIAL.
FT TRANSMEM 422 442 POTENTIAL.
FT CARBOHYD 330 330 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 541 541 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 629 AA; 71996 MW; 2384480E9289C16F CRC64;

Query Match 4.6%; Score 107.5; DB 1; Length 629;
Best Local Similarity 21.7%; Pred. No. 1.4;
Matches 57; Conservative 46; Mismatches 77; Indels 83; Gaps 17;

QY 214 GPVVVAISLAFTEFFLYSFVRDVIHPIYARNOQSDFKYKIEIVNKLPIVAITLLSLVY-L 272
DB 123 GTFVLVMTATLLTYLCFVP---HPFYR-PCAGFGSPPLSV---RAGIMATISLVPFVPSL 175
QY 273 AG-----LAAAYQLYXGTYKRYRFPFWLWLOCRKQLGLLSFFEFAMVHVAYSICLPM 325
DB 176 SKKINVGWLVLSTE-----KINIHQW-----ASILCLFFSWVHV-----IPF 215
QY 326 RRSRYFLFNMAVQOVHANIENSWNEEVEVRIEMYSFGIMSLGLLSLAVTSIP----- 380
DB 216 LRQARH---EGGYRMH---QRWKASDWR-----SCVPPILFNLLWLSLPIARRH 262

```

```

QY 381 --SVSNALNWRREFSIQSTLGYVALLISTFHV-----LIYGWKRAFEYFYR- 425
DB 263 FYEIFLQLHW-----ILAVGEYISLF---YHVPGLNSHMYLVATIVVM---FAQLFYRL 311
QY 426 ---FYTPPNFVLALVLPISVIL 444
DB 312 AVKGLRPRGSRFMASTIANVSIV 334

RESULT 7
FSHR_HUMAN
ID FSHR_HUMAN STANDARD; PRT; 695 AA.
AC P23945;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE FOLLICLE STIMULATING HORMONE RECEPTOR PRECURSOR (FSH-R) (FOLLITROPIN
DE RECEPTOR).
GN FSHR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=OVARY;
RX MEDLINE=91222171; PubMed=1709010;
RA Minegishi T., Nakamura K., Takakura Y., Ibuki Y., Igarashi M.;
RT "Cloning and sequencing of human FSH receptor cDNA.";
RL Biochem. Biophys. Res. Commun. 175:1125-1130(1991).
RN [2]
SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RX MEDLINE=93246012; PubMed=1301382;
RA Kelson C.A., Cheng S.V., Nugent N.P., Schweickhardt R.L.,
RA Rosenthal J.L., Overton S.A., Wands G.D., Kuzeja J.B., Luchette C.A.,
RA Chappel S.C.;
RT "The cloning of the human follicle stimulating hormone receptor and
RT its expression in COS-7, CHO, and Y-1 cells.";
RL Mol. Cell. Endocrinol. 89:141-151(1992).
RN [3]
SEQUENCE FROM N.A.
RA Tilly L.T., Aihara T., Nishimori K., Jai X.-C., Billig H.,
RA Kowalski K.I., Perlman E.A., Hsueh A.J.;
RL Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.
RN [4]
SEQUENCE OF 1-342 FROM N.A.
RC TISSUE=TESTIS;
RX MEDLINE=93075197; PubMed=1359889;
RA Gromoll J., Gudermann T., Nieschlag E.;
RT "Molecular cloning of a truncated isoform of the human follicle
RT stimulating hormone receptor.";
RL Biochem. Biophys. Res. Commun. 188:1077-1083(1992).
RN [5]
SEQUENCE OF 1-51 FROM N.A.
RX MEDLINE=95011044; PubMed=7926278;
RA Gromoll J., Bankbar B., Gudermann T.;
RT "Characterization of the 5' flanking region of the human follicle-
RT stimulating hormone receptor gene.";
RL Mol. Cell. Endocrinol. 102:93-102(1994).
RN [6]
3D-STRUCTURE MODELING OF 49-228.
RX MEDLINE=96363672; PubMed=8747461;
RA Jiang X., Dreano M., Buckler D.R., Cheng S., Ythier A., Wu H.,
RA Hendrickson W.A., el Tayar N.;
RT "Structural predictions for the ligand-binding region of glycoprotein
RT hormone receptors and the nature of hormone-receptor interactions.";
RL Structure 3:1341-1353(1995).
CC -!- FUNCTION: RECEPTOR FOR FOLLICLE STIMULATING HORMONE. THE ACTIVITY
CC OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
CC ADENYLATE CYCLASE.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- ALTERNATIVE PRODUCTS: A SHORT FORM OF THE TESTICULAR PROTEIN IS
CC PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THE SEQUENCE

```

CC SHOWN HERE IS THAT OF THE LONG TESTICULAR PROTEIN.
 CC -!- TISSUE SPECIFICITY: SERTOLI CELLS AND OVARIAN GRANULOSA CELLS.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC FSH/LSH/TSH SUBFAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC
 CC EMBL; M65085; AAA52477.1; -
 CC EMBL; S59000; AAB26480.1; -
 CC EMBL; M95489; AAA52478.1; -
 CC EMBL; X68044; CAA48179.1; -
 CC EMBL; S73199; AAB32071.1; -
 CC PIR; JN0122; JN0122.
 CC DR PDB; 1XUN; 15-MAY-97.
 CC DR GCRDB; GCR_0071; -
 CC DR GCRDB; GCR_0404; -
 CC DR GCRDB; GCR_0588; -
 CC DR GCRDB; GCR_0690; -
 CC DR MIM; 136435; -
 CC DR INTERPRO; IPR000276; -
 CC DR INTERPRO; IPR000372; -
 CC DR INTERPRO; IPR001611; -
 CC DR INTERPRO; IPR002131; -
 CC DR INTERPRO; IPR002272; -
 CC DR PFAM; PF00001; 7tm.1; 1.
 CC DR PFAM; PF00560; LRR; 4.
 CC DR PFAM; PF01462; LRRNT; 1.
 CC DR PRINTS; PR00373; GLYCHORMONER.
 CC DR PRINTS; PR01143; FSHRECEPTOR.
 CC DR PROSITE; PS00237; G-PROTEIN_RECP_FL_1; 1.
 CC DR PROSITE; PS00262; G-PROTEIN_RECP_FL_2; 1.
 CC KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
 KW Phosphorylation; Repeat; Leucine-repeat; Alternative splicing;
 KW 3D-structure.
 FT SIGNAL 1 17
 FT CHAIN 18 695
 FT DOMAIN 18 695
 FT TRANSMEM 367 387
 FT DOMAIN 367 387
 FT TRANSMEM 388 398
 FT DOMAIN 388 398
 FT TRANSMEM 399 421
 FT DOMAIN 399 421
 FT TRANSMEM 422 443
 FT DOMAIN 422 443
 FT TRANSMEM 444 465
 FT DOMAIN 444 465
 FT TRANSMEM 466 485
 FT DOMAIN 466 485
 FT TRANSMEM 486 508
 FT DOMAIN 486 508
 FT TRANSMEM 509 528
 FT DOMAIN 509 528
 FT TRANSMEM 529 550
 FT DOMAIN 529 550
 FT TRANSMEM 551 573
 FT DOMAIN 551 573
 FT TRANSMEM 574 597
 FT DOMAIN 574 597
 FT TRANSMEM 598 608
 FT DOMAIN 598 608
 FT TRANSMEM 609 630
 FT DOMAIN 609 630
 FT TRANSMEM 631 695
 FT DOMAIN 631 695
 FT CARBOHYD 191 191
 FT CARBOHYD 191 191
 FT CARBOHYD 199 199
 FT CARBOHYD 199 199
 FT CARBOHYD 293 293
 FT CARBOHYD 293 293
 FT CARBOHYD 318 318
 FT CARBOHYD 318 318
 FT DISULFID 442 517
 FT DISULFID 442 517
 FT VARSPLIC 224 285
 FT VARSPLIC 224 285
 FT VARSPLIC 342 695
 FT VARSPLIC 342 695
 FT CONFLICT 13 13
 FT CONFLICT 13 13
 FT CONFLICT 112 112
 FT CONFLICT 112 112
 FT CONFLICT 197 198
 FT CONFLICT 197 198
 FT CONFLICT 295 295
 FT CONFLICT 295 295
 FT CONFLICT 307 307
 FT CONFLICT 307 307
 FT CONFLICT 680 680
 FT CONFLICT 680 680
 FT CONFLICT 680 680
 FT CONFLICT 680 680
 FT SEQUENCE 695 AA; 78294 MW; 723B8E71F76D2CD5 CRC64;

Query Match 4.6%; Score 107.5; DB 1; Length 695;
 Best Local Similarity 17.0%; Pred. No. 1.6;
 Matches 84; Conservative 77; Mismatches 148; Indels 185; Gaps 17;
 FSH/LSH/TSH SUBFAMILY.
 QY 79 HEDALTKTNIIFVAIHREHYTSLWDLRHLLVG-----KILIDVSNMR 121
 DB 98 HEIRKANNL-LYINPEAFQNLQYLLISNTGKHLDPVHKIHSKQVLLDIQDNIN 156
 QY 122 INOYPESNAEYLASLFFDSLVKGFNVVSAWALQGPKASQVYICSNNIQARQVIEL 181
 DB 157 IH-----TIENSPVGLSFESVILWL-----NKGIOEIHNCA----- 189
 QY 182 ARQNFIPIDLGSSAREIENLPLRLFTLWRGPVVVAISLATEFFLYSFVROVIHPYAR 241
 DB 190 ---FNGTQDELNLSDNNLEELPNDVFGHAGSPVILDISRTHSLPSYGLNKKLRA 246
 QY 242 NOOSDFYKIPIEIVNKTLP-PIVAITLLSLVY----- 271
 DB 247 RSTYNLKKLP-----TLEKLVALMEASLTYPSSHCCAFANRRROISELHPICNKSILRQE 300
 QY 272 -----LAGLLAAAYQLYGTYKRRF-----PPWLETWLQCRKQL 305
 DB 301 VDMYOTRGQRSSLAEDNESSYRGPDWYTFDYDLNENWVDTCSKPDPAFNPCEIDM 360
 QY 306 G-----LLSFFFAHVHA-----YSLCLPMRKRERYFLNMAVQVHANIE 347
 DB 361 GYNILRVLIWFISLAIITGNTIIVLITTSQYKLTVP-----RELMLNLAFA 408
 QY 348 SWNEEVWRIEMYSFGIMSLGLLSLLAVTSPISVSNALNWR-----FSFIQSTL 398
 DB 409 -----LCIGIYLLIASVDIHTKSOYHNVAIDMQTGAGCDAAGFFTFVASEL 455
 QY 399 G---YVALLISTEH-----VLIYGNKRAPEEYRYFTPPNFV-LA 435
 DB 456 SVYTLTAITLERWHTITHAMQLDCKVOLRRAASVVMGWIFAFAAALFFPIGSIYMKVS 515
 QY 436 LVLPISVILDLQL 449
 DB 516 ICLPMDIDSLSQL 529
 RESULT 8
 ID FSHR_PIG STANDARD; PRT; 695 AA.
 AC P49059; O77514;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE FOLLICLE STIMULATING HORMONE RECEPTOR PRECURSOR (FSH-R) (FOLLITROPIN RECEPTOR).
 GN FSHR.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-OVARY;
 RX MEDLINE-96011644; PubMed-7590277;
 RA Remy J.J., Lahbib-Mansais Y., Verle M., Bozon V., Couture L., Pajot E., Grebert D., Salesse R.;
 RT "The porcine follitropin receptor: cDNA cloning, functional expression and chromosomal localization of the gene.";
 RL Gene 163:257-261(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-OVARY;
 RA Wang Y.F., Meyer K.B., Schmidt K., Wan S.J., Degen S.J.F., La Barbera A.R.;
 RT "Porcine follicle-stimulating hormone receptor.";
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: RECEPTOR FOR FOLLICLE STIMULATING HORMONE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLATE CYCLASE.

Query Match 4.4%; Score 103; DB 1; Length 465;
Best Local Similarity 18.7%; Pred. No. 2.1;
Matches 76; Conservative 64; Mismatches 142; Indels 124; Gaps 16;

QY 110 GKILDSNNMRINQYPSNAEYASLPDSLIIVKGFNNVSAWALQGPDA---SROVY 166
DB 79 GILSSVFFGVVQAP---VCYLSGIYPMKRIIGSSFLSLMSLLIPPAQVGAALVI 135
QY 167 ICSNNIARQOVIELARQNLFI---PIDGLSSLSAREIENLPLRLFTLWRGPPVVV--- 218
DB 136 VCRVLQIAQGVSTGQHEIWKWAPPLERGLTS-----MTLSGFYM--GPFIVLLVS 187
QY 219 -----AISLATEFFLYSFVRDVIHPYARNOQSDF----- 247
DB 188 GFICDLGMPVFIYFIVGCVGLSLSWFFLFFDDPKD--HPYMSSEKDYIIISLMQOAS 245
QY 248 ---YKIPIEIVNKTLPVIAITLS----- 268
DB 246 SGRQSLPIKAMLSLPLWAILNSAFIWSNLLIYTFITSTVLHNVNRENGLLSSLP 305
QY 269 --LVYLAGLLAAAYQLYGTGYRPPMWLETWLOCRKQLGLLSFFFAVHVAYSICLPMR 326
DB 306 YLLAVICGILAGOMDFELTRK-----IFSIVTVRKLTFTLGSCPCPVIFIMCLLVLSYN 359
QY 327 RSEVFLFNMAQQVHANIENSWNEEVRTEM---YISF--GIMSL-----GLLSLLAV 376
DB 360 FYSTVIFLTA-----NSTLSYCYGQILNADIAPIRYGFLKAVTALIGMFGGLISSTLA 415
QY 377 TSIPSVSNALNWFESFIOSTCYVALLISTPHVL-----YXGWR 417
DB 416 GLILLNQDPEYAHKISFLMAGINVTCLV---FYFLFKEAGIOWAK 458

RESULT 11
ID RF3_SACBA STANDARD; PRT; 476 AA.
AC P05512;
DT 01-NOV-1988 (Rel. 09, Created)
DE 01-NOV-1988 (Rel. 09, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE MATURASE-LIKE RF3 PROTEIN.
GN RF3
OS Saccharomyces bayanus (Yeast) (Saccharomyces uvarum).
OG Mitochondrion.
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomyces.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-87280035; PubMed-2440860;
RA Seraphin B., Simon M., Faye G.;
RT "The mitochondrial reading frame RF3 is a functional gene in
Saccharomyces uvarum."
RL J. Biol. Chem. 262:10146-10153(1987).
CC -1- SIMILARITY: THE RF3 PROTEINS ARE RELATED TO THE MATURASES.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
DR EMBL; J03300; CAB23320.1; -
DR PIR; A28439; A28439.
DR INTERPRO; IPR001982;
DR PFAM; PF00961; Intron_maturase; 1.
KW Mitochondrion.
SQ SEQUENCE 476 AA; 57863 MW; ECB416C51DFFDA6D CRC64;

Query Match 4.3%; Score 100; DB 1; Length 476;
Best Local Similarity 20.7%; Pred. No. 3.6;

Matches 52; Conservative 48; Mismatches 85; Indels 56; Gaps 12;

QY 62 NPKFASFEPPHYVDVTHHEDALTQNTI-----IFVAIHREHYT-----SLMD 103
DB 254 NPFYVNAFSINI-----KTNLAKEIFTNKNLYSDYKINQINNHIPIYNYLK 302
QY 104 LRHLVGLKILDSNNMRINQYPSNAEYASLP--PSLIIVKGFNNVSAWALQGPDA 161
DB 303 INNKLPKINMDIKNNYWLAGFTAADGSFLSSWYMPKDTLLFKDM----- 347
QY 162 SROVVICSNICARQOVIELARQNLFIPIIDGLSSLSAREIENLPLRLFTLWRGPPVVVAIS 221
DB 348 -RPSVIS--QVETRELIILOE-----SFDL--SISNVKVGNRKLDKFLFRTTDELKMK 400
QY 222 LATFFFLYSFVRDVIHPYARNOQSDFYKIP-----TEIVNKTLPVIAITLSLVLVLAGLIA 277
DB 401 -----FIYF--DKFLPLHDNKQFNYKFRFTFIKSYNNNRVFCVLSE--YINNIKI 451
QY 278 RAYQLIYYGTKY 288
DB 452 DNYDYIYYNKKY 462

RESULT 12
ID NU4M_BRALA STANDARD; PRT; 452 AA.
AC O79421;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 (EC 1.6.5.3).
GN ND4 OR NAD4 OR NADH4.
OS Branchiostoma lanceolatum (Common lancelet) (Amphioxus).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98292550; PubMed-9628930;
RA Spruyt N., Delarbre C., Gachelin G., Laudet V.;
RT "Complete sequence of the amphioxus (Branchiostoma lanceolatum)
RT mitochondrial genome: relations to vertebrates."
RL Nucleic Acids Res. 26:3279-3285(1998).
CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
DR EMBL; Y16474; CAA76256.1; -
DR INTERPRO; IPR000260; -
DR INTERPRO; IPR001750; -
DR PFAM; PF00361; oxidored_q1; 1.
DR PFAM; PF01059; oxidored_q5_N; 1.
KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SQ SEQUENCE 452 AA; 49940 MW; 4067DB59EC184C7A CRC64;

Query Match 4.2%; Score 99.5; DB 1; Length 452;
Best Local Similarity 20.1%; Pred. No. 3.7;
Matches 95; Conservative 56; Mismatches 139; Indels 183; Gaps 25;

QY 109 VQKIL-----IDVSNMNRINQYPSNAEYASLPDSLIIVKGFNNVSAWALQGPDA 162
DB 29 VGSVLMLPATVTLVNNMTI-----SNVSYMMT---SDFVSLGLTVLSIWLPL-MLLAS 79
QY 163 ROVYICSNNIQAR-----QOVIELARQNLFIPIIDGLSSLSAREIENLPLRLFTLWRGPV 216
DB 80 QQHMVSESIIYQRFVGCQVFTGALVLAFAFMSDLLLFYIAFESTLLPTLIMLTRW-GAQ 138

QY 217 VVAISLAFYFFLYSEVRDVIHPIYARNOQSDFYKIPETVNTKLTPIVATLTLVLAAGLL 276
D 11: : : : :
Db 139 KERYOAGTYFMEFTLV-----GSLPLL-ICLLIGQYQMVGSL 173
QY 277 A-----AAQYLYGTGYKRRPPWLETHLQCRKQLGSLFFFMVHVAYSICLP----- 324
D 11: : : : :
Db 174 ALDLSYEGVQLSYLVNF-----W---WVGC-----ILAFVLKPLGYGVHLWLPKRAHVEA 220
QY 325 -----MRRSERYLEFLNM----- 336
D 11: : : : :
Db 221 PIAGSMVLAVLLKGGYGMVRVSLMNGATAMLSSEVFLALALMGVVMGGICLRQTDLK 280
QY 337 ---AYQQV-----HANIE-----NSWNEEEVWR--- 356
D 11: : : : :
Db 281 SLIAYSSVGHMALVGGVLTCTVANGYCAWVLMIAHGLVSSCLFCLANLWYERSSTRNLS 340
QY 357 --IEWISFGTWSLG--LLSLATVSTPSVS-----NALNWRFSFTQSLTGVAL 403
D 11: : : : :
Db 341 GSRGLMIFPILISLWGLMSLMNMLPAPAINLFGELVAMVALYNWSPSYIVYMSLG--AV 398
QY 404 LISTFPHVLIVG--WKRAFEERYFRY--TPPNFVLAL--VLPSIVILDLQL 449
D 11: : : : :
Db 399 LTAAYSLYLFQMSONGNTM-RNYKNLTITSREYLLTTLHLVPAIYLYFLGL 450

RESULT 13
GP68_HUMAN
ID GP68_HUMAN STANDARD; PRT; 365 AA.
AC Q15743; Q13334;
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE PUTATIVE G PROTEIN-COUPLED RECEPTOR GPR68 (OVARIAN CANCER G PROTEIN-
COUPLED RECEPTOR 1) (OGR-1).
GN GPR68 OR OGR1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-OVARIAN CARCINOMA;
RX MEDLINE=96299795; PubMed=8661159;
RA Xu Y., Casey G.;
RT "Identification of human OGR1, a novel G protein-coupled receptor
that maps to chromosome 14.";
RL Genomics 35:397-402(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA An S., Goetzl E.J.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: ORPHAN RECEPTOR.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: FOUND IN MANY TISSUES, INCLUDING SPLEEN,
TESTIS, PERIPHERAL BLOOD LEUKOCYTES, BRAIN, LUNG, AND PLACENTA.
CC NOT DETECTABLE IN OVARY.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@lsb-sib.ch).
CC
CC EMBL: U48405; AAC50596.1; -
DR EMBL: U35398; AAA79060.1; -
DR GCRDB: GCR_1937; -
DR GCRDB: GCR_1960; -
DR MIM: 601404; -
DR INTERPRO: IPR000276; -
DR PFAM: PF00001; 7tm1; 1.

PRINTS; PR00237; GPCRHHODOPSIN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.
DR PROSITE; PS00262; G-PROTEIN_RECEP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 21 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 22 46 1 (POTENTIAL).
FT DOMAIN 47 58 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 59 80 2 (POTENTIAL).
FT DOMAIN 81 95 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 96 117 3 (POTENTIAL).
FT DOMAIN 118 136 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 137 158 4 (POTENTIAL).
FT DOMAIN 159 183 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 184 205 5 (POTENTIAL).
FT DOMAIN 206 228 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 229 249 6 (POTENTIAL).
FT DOMAIN 250 263 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 264 284 7 (POTENTIAL).
FT DOMAIN 285 365 CYTOPLASMIC (POTENTIAL).
FT DISULFID 94 172 BY SIMILARITY.
FT CARBOHYD 3 3 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 8 8 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 140 140 G -> R (IN REF. 2).
FT CONFLICT 142 142 S -> T (IN REF. 2).
SQ SEQUENCE 365 AA; 41076 MW; 05919AFD5B842CCD CRC64;

Query Match 4.2%; Score 99; DB 1; Length 365;
Best Local Similarity 22.6%; Pred. No. 3.1;
Matches 48; Conservative 37; Mismatches 75; Indels 52; Gaps 9;
QY 255 VNKTLLPVTATLTLVLAAGLAAQYLYGTGYKRRPPWLETHLQCRKQLGSLFFFA 313
D 11: : : : :
Db 19 IQHTLAPVYVTVL-----VVGFPANCLSLYFG-----YLO--IKARNELGVYLCNLT 64
QY 314 MVHVAYSICLPVRRSERYFLNMAVYQQVHANIENSWNEEEVWRIMYSIFGIMSLGLSL 373
D 11: : : : :
Db 65 VADLFYCSLPFW-----LOYVLQHDNWSHGDLSCQVCGILLYENIYI-SVGFLCC 114
QY 374 LAVTSIPSVSNALNWRFSFTQSLTGYYVA-----LLISTF----- 408
D 11: : : : :
Db 115 ISVDRYLAHAPFRFHQFRILKAAGVSVVIAWAKELTSTYFLMHVEEDENQHRVCFE 174
QY 409 HVLHYGNKRAFEERYFYRTPPNFVLALVLP 440
D 11: : : : :
Db 175 HYPIQANQRAI--NYRFLVGLFPLICLLAS 204

RESULT 14
POLG_YEFV1
ID POLG_YEFV1 STANDARD; PRT; 3411 AA.
AC P03314; O42028;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 13-DEC-1998 (Rel. 37, Last annotation update)
DE GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX
PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL
PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED
RNA POLYMERASE (EC 2.7.7.48) (NS5)].
OS Yellow fever virus (strain 17D).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85272570; PubMed=4023707;
RA Rice C.M., Lencches E.M., Eddy S.R., Shin S.J., Sheets R.L.,
RA Strauss J.H.;
RT "Nucleotide sequence of yellow fever virus: Implications for
flavivirus gene expression and evolution.";
RL Science 229:726-733(1985).
CC -!- FUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARE
HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCTION.
CC NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION.

